NEB 1233

```
      -1391      -1381      -1371      -1361      -1351      -1341      -1331      -1321
        *          *          *          *          *          *          *          *
  AGCGGATAAC AATTTCACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTTGGTACC GAGCTCGGAT CCACTAGTAA
                                              pCR2.1                         -BamHI-      >
  _____ Lac promoter _____>
```

```
      -1311      -1301      -1291      -1281      -1271      -1261      -1251      -1241
        *          *          |*         *          *          *          *          *
  CGGCCGCCAG TGTGCTGGAA TTCGGCTTAC TATAGGGCAC GCGTGGTCGA CGGCCCGGGC TGGTAACTTT AAGAGAAATT
             pCR2.1                          >                  -SmaI-
                      _____GenomeWalker Adaptor_____>
                                                            _____cmACO1_____>
```

```
      -1231      -1221      -1211      -1201      -1191      -1181      -1171      -1161
        *          *          *          *          *          *          *          *
  GGTAAAATTC CTAGAGAGAA TTGTAATTAA TATAGGAGAA TGATTTTAAT TCTAATGTTG TATCCATTTT CGATAAAGTT
                              cmACO1 Genomic DNA                                        >
```

```
      -1151      -1141      -1131      -1121      -1111      -1101      -1091      -1081
        *          *          *          *          *          *          *          *
  AAATAAAGTG TCGTAGACGA CCATCATTCT TAATCCATTT GTACTTATCA AATTTGTATC TGAGATTTAA GTTCAAATTC
                              cmACO1 Genomic DNA                                        >
```

```
      -1071      -1061      -1051      -1041      -1031      -1021      -1011      -1001
        *          *          *          *          *          *          *          *
  ACACTAAAAC AATCGAAATG TATGCGACAA TCACAATGGA AAATACGTAT GATGTATTCC ATCACCTTTC AAGTTCTAAC
                              cmACO1 Genomic DNA                                        >
```

```
       -991       -981       -971       -961       -951       -941       -931       -921
        *          *          *          *          *          *          *          *
  CTAGGATATG TTTTGGAATA TTTGAGATTT ATTAAAATTAT TCTTTTATCC GTTGACAGTT TATTTTTTGT TTAACGATGT
                              cmACO1 Genomic DNA                                        >
```

```
       -911       -901       -891       -881       -871       -861       -851       -841
        *          *          *          *          *          *          *          *
  ATGTAAGAAA CGACGAAATA TGTGATTAAA CCAAGATCGC ATACAAATAA GAGCTAGATC CTAAAGATAT ATAAAAGTAT
                              cmACO1 Genomic DNA                                        >
```

```
       -831       -821       -811       -801       -791       -781       -771       -761
        *          *          *          *          *          *          *          *
  GATCAACAAC GTACAAAACG TTTCTTTTCG ATGATAATTA TCTTAAGAAC TTCAAGGTTA ATTTAGATCT CTTAATTAAA
                              cmACO1 Genomic DNA                                        >
```

```
       -751       -741       -731       -721       -711       -701       -691       -681
        *          *          *          *          *          *          *          *
  AAATTTCATA GATAATGCAT CCGTGAACAA GAAAAAACAT AAAGAACCCA TGGTTGTCCT AATTTTTGTA GTAAATAAGC
                              cmACO1 Genomic DNA                                        >
```

```
-671   -661       -651       -641       -631       -621       -611       -601
        *          *          *          *          *          *          *          *
  GTAGTTCAAG ACACAAGTAA GAATGACGTT ACCACATGTT AATCTAGATT CCAAAACTTG AGCTTGAGAG CACGTTACGA
                              cmACO1 Genomic DNA                                        >
```

Fig. 1A

```
        -591        -581        -571        -561        -551        -541        -531        -521
          *           *           *           *           *           *           *           *
AAATAATCTA CGAAAACGAG TAAGTCGTCT AAGTTCGTTT TCGTTTATTT GACACGTAAG ATACTCGTAT TGAAAGAAGA
_____cmACO1 Genomic DNA_____>

        -511        -501        -491        -481        -471        -461        -451        -441
          *           *           *           *           *           *           *           *
CGAAAAATGG AAAAAAGTAA AGAAGGTAAG GAGGTGGGTG AGTCCAAAGG AAACATACCA AATTCATGCA AGAACTATGA
_____cmACO1 Genomic DNA_____>

        -431        -421        -411        -401        -391        -381        -371        -361
          *           *           *           *           *           *           *           *
GATTCAGAAA TTAAGAGAAA AGTGTGGAAA TCATGTAACT AAATTTAAAA TACATATAGG TACTATTTTC TTTCCTTTTC
_____cmACO1 Genomic DNA_____>

        -351        -341        -331        -321        -311        -301        -291        -281
          *           *           *           *           *           *           *           *
TATTGAAACA AAGAGACCAA GGGGGAATTA GGGTATATGG CATTGGCAGA CATAAAAATA ATAAAGTTAA ATCAAATTGG
_____cmACO1 Genomic DNA_____>

        -271        -261        -251        -241        -231        -221        -211        -201
          *           *           *           *           *           *           *           *
GTCCCAAACT CACCAAAGAG GAAATTCAGT GTTGAATAAA GCCAATTAGC CAAAGCCAAA GCCAAAGCCA CCTCCTCTCT
_____cmACO1 Genomic DNA_____>

        -191        -181        -171        -161        -151        -141        -131        -121
          *           *           *           *           *           *           *           *
TTCCCACATA CATGCATGAA ATTTCATGGG CCCATTCTTT TTATCATCAC ATTTTTAATA ATTTTATCTT CTTCTTCTTC
_____cmACO1 Genomic DNA_____>

        -111        -101         -91         -81         -71         -61         -51         -41
          *           *           *           *           *           *           *           *
TTCTTCTTCT TCTTCTTCTT CTTCTTCTTC TTCTTCTTCT TTTTTTAATC AATTTCTTCC CACTTTCCAA TCCTAAATAA
_____cmACO1 Genomic DNA_____>


TATA box
  |
        -31         -21         -11          -1          10          20          30          40
  | *           *           *           *           *           *           *           *
ATTTCACTAT AAATACCCCT TCATTATAAC TTGATCCAAC ACACCCACCA ACCAAAAACA AAACCTTGAT ACCAAAGAGT
_____cmACO1 Genomic DNA_____>


                                                                <Aco1ProR-a
         50          60          70          80          90                 |
          *           *           *           *           *                 |
TCTTTTTTCT TTATTTGCAC AAACCAAATC TTGTATCTAC AAAAAGAAAT GGCTGTCTA
                  TAG AACATAGATG TTTTTCTTcc taGgCAGAT
                                                       -BamHI-
_____cmACO1 Genomic DNA_____>
```

Fig. 1B

```
        -1289       -1279       -1269       -1259       -1249       -1239       -1229       -1219
          *           *           *           *           *           *           *           *
      AGGAAACAGC  TATGACCATG  ATTACGCCAA GCTTAAGAGA  AATTGGTAAA  ATTCCTAGAG  AGAATTGTAA  TTAATATAGG
                                          HindIII
      _____pUC19_____
                                      _____cmACO1 Genomic DNA_____>

        -1209       -1199       -1189       -1179       -1169       -1159       -1149       -1139
          *           *           *           *           *           *           *           *
      AGAATGATTT  TAATTCTAAT  GTTGTATCCA  TTTTCGATAA  AGTTAAATAA  AGTGTCGTAG  ACGACCATCA  TTCTTAATCC
      _____cmACO1 Genomic DNA_____>

        -1129       -1119       -1109       -1099       -1089       -1079       -1069       -1059
          *           *           *           *           *           *           *           *
      ATTTGTACTT  ATCAAATTTG  TATCTGAGAT  TTAAGTTCAA  ATTCACACTA  AAACAATCGA  AATGTATGCG  ACAATCACAA
      _____cmACO1 Genomic DNA_____>

        -1049       -1039       -1029       -1019       -1009       -999        -989        -979
          *           *           *           *           *           *           *           *
      TGGAAAATAC  GTATGATGTA  TTCCATCACC  TTTCAAGTTC  TAACCTAGGA  TATGTTTTGG  AATATTTGAG  ATTTATTAAA
      _____cmACO1 Genomic DNA_____>

        -969        -959        -949        -939        -929        -919        -909        -899
          *           *           *           *           *           *           *           *
      TTATTCTTTT  ATCCGTTGAC  AGTTTATTTT  TTGTTTAACG  ATGTATGTAA  GAAACGACGA  AATATGTGAT  TAAACCAAGA
      _____cmACO1 Genomic DNA_____>

        -889        -879        -869        -859        -849        -839        -829        -819
          *           *           *           *           *           *           *           *
      TCGCATACAA  ATAAGAGCTA  GATCCTAAAG  ATATATAAAA  GTATGATCAA  CAACGTACAA  AACGTTTCTT  TTCGATGATA
      _____cmACO1 Genomic DNA_____>

        -809        -799        -789        -779        -769        -759        -749        -739
          *           *           *           *           *           *           *           *
      ATTATCTTAA  GAACTTCAAG  GTTAATTTAG  ATCTCTTAAT  TAAAAAATTT  CATAGATAAT  GCATCCGTGA  ACAAGAAAAA
      _____cmACO1 Genomic DNA_____>

        -729        -719        -709        -699        -689        -679        -669        -659
          *           *           *           *           *           *           *           *
      ACATAAAGAA  CCCATGGTTG  TCCTAATTTT  TGTAGTAAAT  AAGCGTAGTT  CAAGACACAA  GTAAGAATGA  CGTTACCACA
      _____cmACO1 Genomic DNA_____>

        -649        -639        -629        -619        -609        -599        -589        -579
          *           *           *           *           *           *           *           *
      TGTTAATCTA  GATTCCAAAA  CTTGAGCTTG  AGAGCACGTT  ACGAAAATAA  TCTACGAAAA  CGAGTAAGTC  GTCTAAGTTC
      _____cmACO1 Genomic DNA_____>

        -569        -559        -549        -539        -529        -519        -509        -499
          *           *           *           *           *           *           *           *
      GTTTTCGTTT  ATTTGACACG  TAAGATACTC  GTATTGAAAG  AAGACGAAAA  ATGGAAAAAA  GTAAAGAAGG  TAAGGAGGTG
      _____cmACO1 Genomic DNA_____>
```

Fig. 2A

```
        -489       -479       -469       -459       -449       -439       -429       -419
          *          *          *          *          *          *          *          *
     GGTGAGTCCA AAGGAAACAT ACCAAATTCA TGCAAGAACT ATGAGATTCA GAAATTAAGA GAAAAGTGTG GAAATCATGT
     _____cmACO1 Genomic DNA_____>


        -409       -399       -389       -379       -369       -359       -349       -339
          *          *          *          *          *          *          *          *
     AACTAAATTT AAAATACATA TAGGTACTAT TTTCTTTCCT TTTCTATTGA AASRAAGAGA NNAAGGGGGA ATTAGNGTAT
     _____cmACO1 Genomic DNA_____>


        -329       -319       -309       -299       -289       -279       -269       -259
          *          *          *          *          *          *          *          *
     ATGGCATTGG CAGACATAAA AATAATAAAG TTAAATCAAA TTGGGTCCCA AACTCACCAA AGAGGAAATT CAGTGTTGAA
     _____cmACO1 Genomic DNA_____>


        -249       -239       -229       -219       -209       -199       -189       -179
          *          *          *          *          *          *          *          *
     TAAAGCCAAT TAGCCAAAGC CAAAGCCAAA GCCACCTCCT CTCTTTCCCA CATACATGCA TGAAATTTCA TGGGCCCATT
     _____cmACO1 Genomic DNA_____>


        -169       -159       -149       -139       -129       -119       -109        -99
          *          *          *          *          *          *          *          *
     CTTTTTATCA TCACATTTTT AATAATTTTA TCTTCTTCTT CTTCTTCTTC TTCTTCTTCT TCTTCTTCTT CTTCTTCTTC
     _____cmACO1 Genomic DNA_____>


                                                                    TATA box
         -89        -79        -69        -59        -49  |     -39        -29        -19
          *          *          *          *          *   |      *          *          *
     TTCTTTTTTT AATCAATTTC TTCCCACTTT CCAATCCTAA ATAAATTTCA CTATAAATAC CCCTTCATTA TAACTTGATC
     _____cmACO1 Genomic DNA_____>


                      transcriptional start site in Tomato E4
                             |
          -9        |2        12          translational start site
          *         |*         *          |
     CAACACACCC AGGATCCATT ATTAGAGATT GAGCC ATGG
                 BamH1
     __cmACO1__          ___Tom E4 5'UTR___
```

Fig. 2B

NEB 1233

```
        -1669      -1659      -1649      -1639      -1629      -1619      -1609      -1599
|         *          *          *          *          *          *          *          *
|
    AGCGGATAAC AATTTCACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTTGGTACC GAGCTCGGAT CCACTAGTAA
                                                            HindIII              -BamHI-
    _____Lac promoter_____>
    _____pCR2.1_____>

        -1589      -1579      -1569      -1559      -1549      -1539      -1529      -1519
          *          *          *          *          *          *          *          *

    CGGCCGCCAG TGTGCTGGAA TTCGGCTTGT AATACGACTC ACTATAGGGC ACGCGTGGTC CACGGCCCGG GCTGGTAACT
    _____pCR2.1_____>
                        _____GenomeWalker Adaptor_____>
                                                                            ___>

        -1509      -1499      -1489      -1479      -1469      -1459      -1449      -1439
          *          *          *          *          *          *          *          *

    AGAAGCTAAA GGACGACGTC AACATAATTA AAATTACTCC AAGATAATTA AAATTAAAAA TATCTTATAT TTTATGGCGT
    _____MEL7 promoter_____>

        -1429      -1419      -1409      -1399      -1389      -1379      -1369      -1359
          *          *          *          *          *          *          *          *

    TACATCTTCC TTTCCTCTTC TTCTTTTTTC TGCTGCGATT TCTTCCCATC TATTTCTTCT TTTACTCTTA TTTTTTTCTT
    _____MEL7 promoter_____>

        -1349      -1339      -1329      -1319      -1309      -1299      -1289      -1279
          *          *          *          *          *          *          *          *

    TACATTGTTT AGATTTGGGT AACCAAATCT GATTTCTTTC TATCGTCTTT CTTCTTTTTC TCTTTTTTTT TCCGCTGCGA
    _____MEL7 promoter_____>

    -1269      -1259      -1249      -1239      -1229      -1219      -1209      -1199
      *          *          *          *          *          *          *          *

    TTTCTTCCCA TTGTCTATCG TTTTTTCCTC TTTTTTTTTT TACATCGTAA CCAAATCTAA AAGATCGTAT ATAAAGAATC
    _____MEL7 promoter_____>

        -1189      -1179      -1169      -1159      -1149      -1139      -1129      -1119
          *          *          *          *          *          *          *          *

    TTCAAAAAAA AAAATTGTTT AGATTGGAGT AGCCAAATTT AAACAATCGC GTAAAAAAAA TAAACGATCG TAGACAAATC
    _____MEL7 promoter_____>

        -1109      -1099      -1089      -1079      -1069      -1059      -1049      -1039
          *          *          *          *          *          *          *          *

    TAAACGATCG TGCACAAAAA GATTTAAAAA AATCGTTTAG TCAAATCTAA ACAATTGTAT AACCAAATTA AACGATAGAA
    _____MEL7 promoter_____>

        -1029      -1019      -1009       -999       -989       -979       -969       -959
          *          *          *          *          *          *          *          *

    TTGAAATAAT AAATCGGTTA GATTTGGCTA TCCAAATTTA AATGACCAAA TCTAAACGAT CGTATACCAA ATCTAAACGA
    _____MEL7 promoter_____>
```

Fig. 3A

```
        -949        -939        -929        -919        -909        -899        -889        -879
         *           *           *           *           *           *           *           *
    TCGKATACCA  AATCTAAATG  ATCATGTACC  AAATATATTA  TGCACATTGT  TGGCAGGGTG  GTTGACGGAA  CATTTTGTAT
    _____MEL7 promoter_____>


        -869        -859        -849        -839        -829        -819        -809        -799
         *           *           *           *           *           *           *           *
    ATTTTCTATT  ATGGGTTTGT  AGAATTTTTT  CATTTTCGAA  ATTGTTCTAT  ACAATATAAA  TATAAATATT  TTACCACTTC
    _____MEL7 promoter_____>


        -789        -779        -769        -759        -749        -739        -729        -719
         *           *           *           *           *           *           *           *
    GTTATATTTT  CGAAAGACC   CCTTAAATAA  ATTGAATTCG  CATATAATTA  AAATTTTTTC  CCAAAAAAAG  TAGACTATGT
    _____MEL7 promoter_____>


        -709        -699        -689        -679        -669        -659        -649        -639
         *           *           *           *           *           *           *           *
    CTATCTAAAA  ATTTGATTCC  CAATATAGAA  CAAATTCTCA  AAATGAACAA  ACATTTGAAA  TTCTCGATAT  AGAAAACATT
    _____MEL7 promoter_____>


        -629        -619        -609        -599        -589        -579        -569        -559
         *           *           *           *           *           *           *           *
    TACTTATTTT  GAATTGGGAC  ATATTCCAAA  GTTTATTCCA  AACGTAACTT  TGAAGGAAAA  GTTGATTGAG  ATTACATCCA
    _____MEL7 promoter_____>


        -549        -539        -529        -519        -509        -499        -489        -479
         *           *           *           *           *           *           *           *
    TATTTTTGTT  TTTCATATTG  AATTTCATGG  AAAATTAAAA  TGCACACAAA  ATGATGTATG  AGATTAAACC  AAAGTTTATC
    _____MEL7 promoter_____>


        -469        -459        -449        -439        -429        -419        -409        -399
         *           *           *           *           *           *           *           *
    GTTATTGAAT  TCTTTTATTA  AAAAACCAAC  AAAATTTTAA  AACTTGTTTG  CAATAGACCA  ATATAGTTAA  TCCATCGTGG
    _____MEL7 promoter_____>


        -389        -379        -369        -359        -349        -339        -329        -319
         *           *           *           *           *           *           *           *
    TCTATTGTAG  ATAAATTGTA  ATATTTTGTT  ATATTTAATA  AATATTTTGA  TTTATTTTGA  TATATTTGTA  TTTAGATAAC
    _____MEL7 promoter_____>


        -309        -299        -289        -279        -269        -259        -249        -239
         *           *           *           *           *           *           *           *
    AAAATTAAGA  TTTAAATATT  ATTTTATATC  TTAATATAAA  CATTTGTTAA  TTTTTTCTAT  TTTAGACCAT  TTCTCTTATT
    _____MEL7 promoter_____>


        -229        -219        -209        -199        -189        -179        -169        -159
         *           *           *           *           *           *           *           *
    TTTATATAAC  ATTTTAATAA  CTAAATGATG  TGACACACAC  TAATATTATT  TTTATCCAAA  GAAAATAATG  CTATAAAATA
    _____MEL7 promoter_____>
```
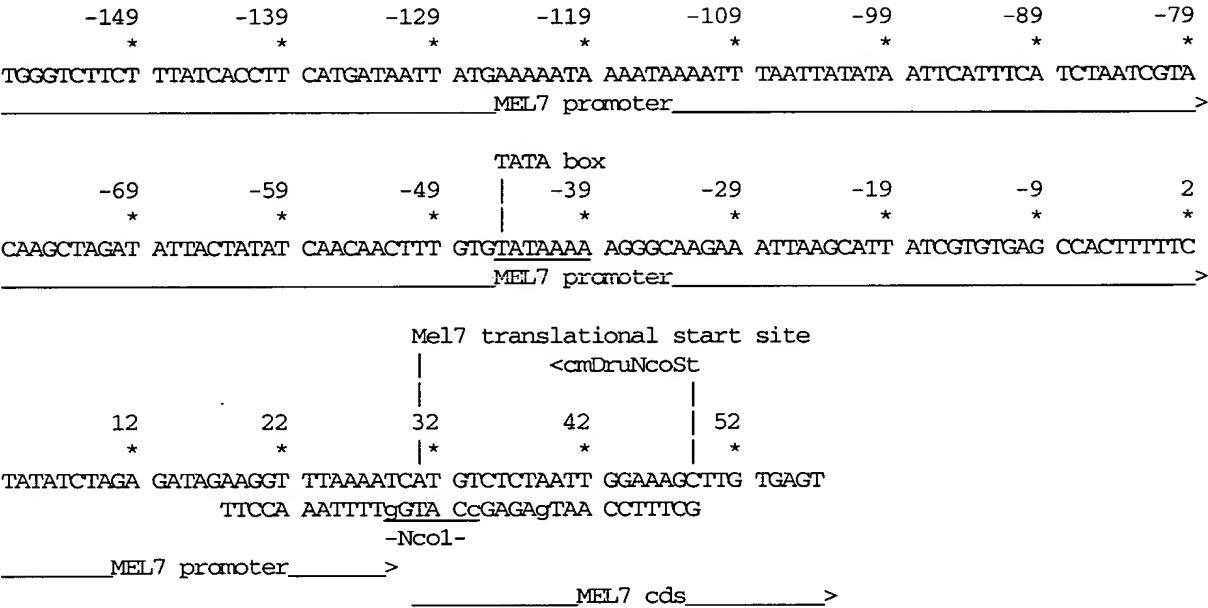
Fig. 3B

```
        -149       -139       -129       -119       -109        -99        -89        -79
          *          *          *          *          *          *          *          *
      TGGGTCTTCT TTATCACCTT CATGATAATT ATGAAAAATA AAATAAAATT TAATTATATA ATTCATTTCA TCTAATCGTA
      _____MEL7 promoter_____>


                                                   TATA box
         -69        -59        -49        |  -39       -29        -19         -9          2
          *          *          *         |   *          *          *          *          *
      CAAGCTAGAT ATTACTATAT CAACAACTTT GTGTATAAAA AGGGCAAGAA ATTAAGCATT ATCGTGTGAG CCACTTTTTC
      _____MEL7 promoter_____>


                                    Mel7 translational start site
                                          |          <cmDruNcoSt
                                          |                        |
          12         22         32        |  42        |  52
          *          *         |*          *          | *
      TATATCTAGA GATAGAAGGT TTAAAATCAT GTCTCTAATT GGAAAGCTTG TGAGT
                   TTCCA AATTTTgGTA CcGAGAgTAA CCTTTCG
                                   -NcoI-
      _____MEL7 promoter_____>
                                     _____MEL7 cds_____>
```

Fig. 3C

```
                         NEB 1233
                            |
         -2158   -2148   -2138   -2128   -2118   -2108   -2098   -2088
           *     |  *       *       *       *       *       *       *
        TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GCCAAGCTTG GTACCGAGCT
                                                             pCR2.1_____>
        _____Lac promoter_____>

         -2078   -2068   -2058   -2048   -2038   -2028   -2018   -2008
           *       *       *       *       *       *       *       *
        CGGATCCACT AGTAACGGCC GCCAGTGTGC TGGAATTCGG CTTACTATAG GGCACGCGTG GTCGACGGCC CGGGCTGGTC
            -SpeI--
        _____pCR2.1_____>
                                               _____GenomeWalker Adaptor_____>
                                                                                       _>

         -1998   -1988   -1978   -1968   -1958   -1948   -1938   -1928
           *       *       *       *       *       *       *       *
        CAATCACCGA ACATCATGTT ATGTAGGTGT CGGGAGATGC TACCTATCTG CTGATGTTGG TTTCTTTCTT TGAAAGATAC
                                        MEL2 promoter_____>

         -1918   -1908   -1898   -1888   -1878   -1868   -1858   -1848
           *       *       *       *       *       *       *       *
        TCTCCTGACT TTTTAGTTGT TGCATCTAGA GATGTCCTCT ATTATTTTGA CACCTTTTCT TCTGACGGTG TAGAGCAACA
                                        MEL2 promoter_____>

         -1838   -1828   -1818   -1808   -1798   -1788   -1778   -1768
           *       *       *       *       *       *       *       *
        CAAAAAAATC TTGAATTTCT ATTAATGGAA TGAGCTATAT CTATACAAAT TGGAACCATA TGACAAATTA AGAAGATTCC
                                        MEL2 promoter_____>

         -1758   -1748   -1738   -1728   -1718   -1708   -1698   -1688
           *       *       *       *       *       *       *       *
        TTTCTGAATA TTATGCAATA GAAATACTCA CCAGGTGTAA TGATGCACCT TATAGAGAAA ACTTCGACGA ACAAGAGACG
                                        MEL2 promoter_____>

         -1678   -1668   -1658   -1648   -1638   -1628   -1618   -1608
           *       *       *       *       *       *       *       *
        GCTACTAAGT TTTAGTAGAA TGGGTATTTC TGACCTACTA TGTTTCAGGA TGCGAGGATC TTCATGGTCA ATTGTGACCG
                                        MEL2 promoter_____>

         -1598   -1588   -1578   -1568   -1558   -1548   -1538   -1528
           *       *       *       *       *       *       *       *
        ATGGTGGAGA ACTGAAAATA TTTCCCATCT CAATGAAATA CTAAAACAAC ATATCTTAGA GGTTGAACTA TTTGATATCT
                                        MEL2 promoter_____>

         -1518   -1508   -1498   -1488   -1478   -1468   -1458   -1448
           *       *       *       *       *       *       *       *
        AGGGAATACA TTTTATGGGA CCGTTTTCTA GTTGTTCCGG CAAACACGCA TTCGAGACGG GACGTTCATG TCGCATACCA
                                        MEL2 promoter_____>
```

Fig. 4A

```
      -1438      -1428      -1418      -1408      -1398      -1388      -1378      -1368
        *          *          *          *          *          *          *          *
    CGGAGGATCC GCATGTAAGC TATCCAAGCA ATACTTCTAC CCTTTTTGTC TTCTTTAATA ATATATTTTT TACTTACTAA
    _____MEL2 promoter_____>


      -1358      -1348      -1338      -1328      -1318      -1308      -1298      -1288
        *          *          *          *          *          *          *          *
    GATAGTTTCT AAATTTGTTG TAGAATCGAA TGCTGGAACT TCAGTCCTAG CTTACCTCAG TGGGTACTTA GCCACTCTCT
    _____MEL2 promoter_____>


      -1278      -1268      -1258      -1248      -1238      -1228      -1218      -1208
        *          *          *          *          *          *          *          *
    GGGGACAAGA TATGCGAGAT GGCGTTGGAT AGACGATTGG ACTACTCAAA AGGCCTTGGT TGGGGACCTA AGTCTAGGGC
    _____MEL2 promoter_____>


      -1198      -1188      -1178      -1168      -1158      -1148      -1138      -1128
        *          *          *          *          *          *          *          *
    CCACAAGACG GCCAGTGTGA GTAGTTCCAC GACCTCATGT TTGTAGTCCA CGGTAGAGCT CCAATTATGG ACTAAGCTTG
    _____MEL2 promoter_____>


      -1118      -1108      -1098      -1088      -1078      -1068      -1058      -1048
        *          *          *          *          *          *          *          *
    ATCAAGCTGT GCAACGGATT GAAGAACAAA CAAGAAATCA CGATGCGTTA GCTTCAAAAG TGGAATGAAT GTGAAAGTTC
    _____MEL2 promoter_____>


      -1038      -1028      -1018      -1008       -998       -988       -978       -968
        *          *          *          *          *          *          *          *
    ATAGAAGACA TGAGTCGGGC ACAGTAAGGA CCACAACATT ATCTTTAGCT TTGCGATACG TATANNTATT TCCATTATTC
    _____MEL2 promoter_____>


       -958       -948       -938       -928       -918       -908       -898       -888
        *          *          *          *          *          *          *          *
    TTAAGTTTTT GAATTACAGT ATTCAGTGAT GATATGCATA TATATGTACC AAACGTAGCC ACTTTTGTAT AATTGTAGGA
    _____MEL2 promoter_____>


       -878       -868       -858       -848       -838       -828       -818       -808
        *          *          *          *          *          *          *          *
    CCTGTGGTGT AGAATGGCAT ATGAGGCTCG TTAAAAGACA TACGATTTTC TTTGTGCTTT TTTTAACGAG GAATATTTTT
    _____MEL2 promoter_____>


       -798       -788       -778       -768       -758       -748       -738       -728
        *          *          *          *          *          *          *          *
    TATTTGTATT ATGAACTTTA TTACATTTCT TGAATTTCTT TGTATTATGA AGATTTAATT TTTTGTTGAA TTTTTGTTTG
    _____MEL2 promoter_____>


       -718       -708       -698       -688       -678       -668       -658       -648
        *          *          *          *          *          *          *          *
    TATTTTGTAA TTTACTAATT TATTTTAAAT TTTCTTTAAT TGAATCGATA ACGAATGCAA ATATTTTACG AAAAAAACTT
    _____MEL2 promoter_____>
```

Fig. 4B

```
        -638        -628        -618        -608        -598        -588        -578        -568
          *           *           *           *           *           *           *           *
    ATAGGAAAAT ATTTCAAAAA AATAAAAAAT TACATATTTA AAATATTTTT CGACGCATTA CATATGTGGA AAATATGGTG
    _____MEL2 promoter_____>

        -558        -548        -538        -528        -518        -508        -498        -488
          *           *           *           *           *           *           *           *
    CAAACATCAC ATCGGGGATG GTTATTACCG ACGCATGAAT GACACCGAAT ATATAAACGT AAGGAATAGT TATTCCTGAC
    _____MEL2 promoter_____>

        -478        -468        -458        -448        -438        -428        -418        -408
          *           *           *           *           *           *           *           *
    GCATAACTGC TGTCGGAACT GTGGAAGTTA GTTCTCGACA TTATTAACAC TTACGTCGAC GTTTTTATGC ATCGGGAGTC
    _____MEL2 promoter_____>

        -398        -388        -378        -368        -358        -348        -338        -328
          *           *           *           *           *           *           *           *
    GCTCCACTTC TTGTAGTGAA GAAATTTTGC CTATAATGTC GGTTTAAAAC CGACATTAAA GGCCAAATTT CTTCTAGTGC
    _____MEL2 promoter_____>
    _____Imperfect inverted repeat_____

        -318        -308        -298        -288        -278        -268        -258        -248
          *           *           *           *           *           *           *           *
    ATAATCAATA TMCAAAAGTT CAATTCCAAA AATTACATTT CTCTAGAAAT TCCGTGTGAA CAATTGTCAT AAAGGTTTTA
    _____MEL2 promoter_____>

        -238        -228        -218        -208        -198        -188        -178        -168
          *           *           *           *           *           *           *           *
    AGTGAATTGA AAATTTCAAA ACGTAATTGG ATTAAGCGAG AAAATTATTT TAATCACCAT TCAAAAGTTA TTAACAATGA
    _____MEL2 promoter_____>

        -158        -148        -138        -128        -118        -108         -98         -88
          *           *           *           *           *           *           *           *
    AAAATATGGA AGATAAGATT TCAAAATTAC GTAATTTACT TCTACGTTTC TTTCTTTCCC CTTTAGTAAC TTCACTCATA
    _____MEL2 promoter_____>

    TATA box
    |    -78         -68         -58         -48         -38         -28         -18          -8
    |      *           *           *           *           *           *           *           *
    TCTTTATATA CGTTCCATCC CTTCACATTC TCATACAAAA TTCTCTTTCA ATATCAACTC TCCTCTCTTA ACTCACCCTT
    _____MEL2 promoter_____>

            MEL2 translational start site
            |           <MEL2_Nco_R
            1 3              13    |
            * *               *    |
    TTTTCAAATG GAAACAATGC AAAC
     AAAGggTAC CTTTGTTACG TTTG
        -NcoI--
    __pro__
          _____MEL2 cds_____
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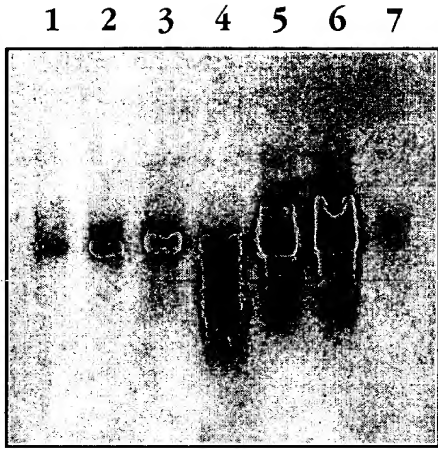
Fig. 4C

Fig. 5A
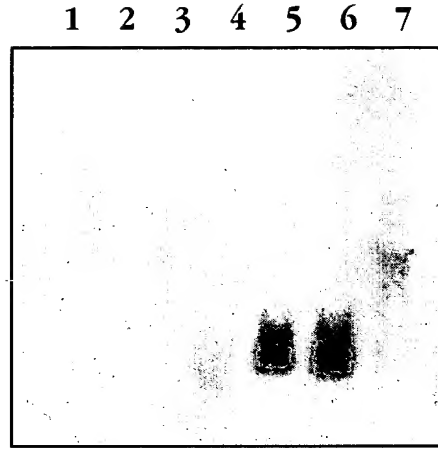
Fig. 5C
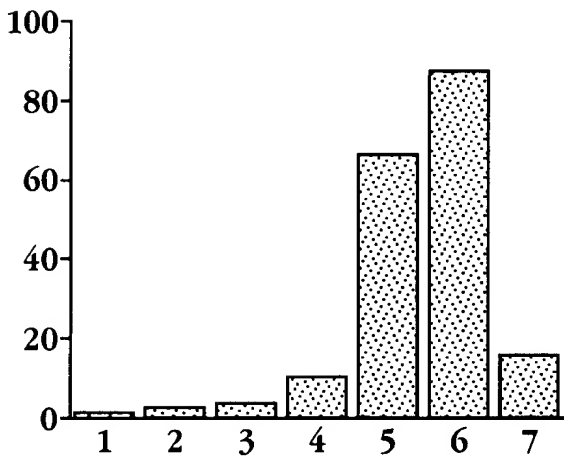
Fig. 5B
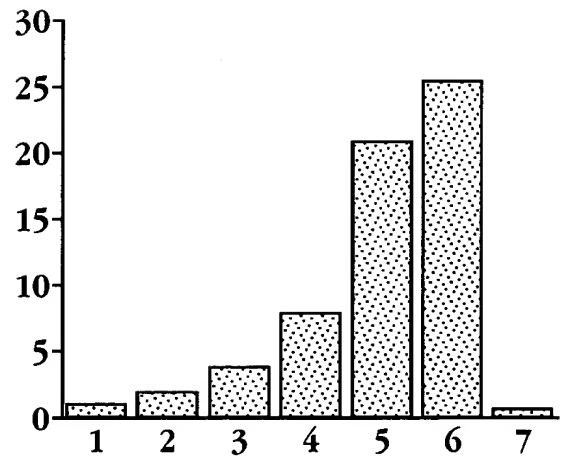
Fig. 5D

```
        -968        -958        -948        -938        -928        -918        -908        -898
         *           *           *           *           *           *           *           *
TGGAATTGTG AGCGGATAAC AATTTCACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTTGGTACC GAGCTCGGAT
                                                                                  BamHI>
_____pCR2.1_____>
_____Lac promoter_____>

        -888        -878        -868        -858        -848        -838        -828        -818
         *           *           *           *           *           *           *           *
CCACTAGTAA CGGCCGCCAG TGTGCTGGAA TTCGGCTTAC TATAGGGCAC GCGTGGTCGA CGGCCCGGGC TGGTAAATTT
_____pCR2.1_____
                                             _____GenomeWalker Adaptor_____>
                                                                                 __6E__>

        -808        -798        -788        -778        -768        -758        -748        -738
         *           *           *           *           *           *           *           *
TGAAAAGTTA GGAGATATTT TTTACATATA AGAGATATTT TTTATAATGT AACATTTTTT TTACTAGACG GTTGAGTCGA
_____6E melon genomic DNA_____>

        -728        -718        -708        -698        -688        -678        -668        -658
         *           *           *           *           *           *           *           *
GTTAGGTTAA AGAAAGGAAA ACTATAAAAT AATTTTTAAT TATTAAATAC ATAAACAATA CTTTGTATTC TATATTAATT
_____6E melon genomic DNA_____>

        -648        -638        -628        -618        -608        -598        -588        -578
         *           *           *           *           *           *           *           *
AAAATGACTA TTGAATTGTT AAGATGTAGG TATCTAAGGA CAAGAAGTCT CGAGTTCAAA TCTTCAACCT CAAAATATAC
_____6E melon genomic DNA_____>

        -568        -558        -548        -538        -528        -518        -508        -498
         *           *           *           *           *           *           *           *
TGCAAGATAG TAACTAATGA ATTATATTTG ACTAAATCAT GTAGCAAAAG AAAATCAAAT TTATCATGTT AAATATGGTC
_____6E melon genomic DNA_____>

        -488        -478        -468        -458        -448        -438        -428        -418
         *           *           *           *           *           *           *           *
AAGCCGGAGC ATTAACAACA ACAATTCATA TTTGTGGTTG ATAGTACTTG ACTAGAATTT AGAGAGTACT TGACTAGAAT
_____6E melon genomic DNA_____>

        -408        -398        -388        -378        -368        -358        -348        -338
         *           *           *           *           *           *           *           *
AAAAATTGGG GGACCCACTA CGACGTCAGC TTGCCTTGCT TAGCAATTAA GCTATCACCT CTTAGTCTAT AGCTTCGTGC
_____6E melon genomic DNA_____>
```

Fig. 6A

```
         -328        -318        -308        -298        -288        -278        -268        -258
          *           *           *           *           *           *           *           *
       GCTGCATTAA  ACGGTATTCT  CACACTTTTC  TTTTCTTTTT  ACCGCACCCG  TCCGGTTAAT  GGCTCCCCCA  CTTTTTACCT
       _____6E melon genomic DNA_____>

         -248        -238        -228        -218        -208        -198        -188        -178
          *           *           *           *           *           *           *           *
       TCCCCGAATC  CACGCCAGTT  GCCAACATGC  GAAGCAGCAA  GTACAATATT  GTCATTTTGC  ATTAACCAAA  ATGACACGTC
       _____6E melon genomic DNA_____>

                                                                                         TATA

                                                                                          |
         -168        -158        -148        -138        -128        -118        -108        -98
          *           *           *           *           *           *           *        | *
       GGATGTCATT  TATGTAATTA  AGCTACAAAG  CCACGGTTAG  TTTCCGAACC  CCCACGATCC  AGTACTTACG  TGTCTCCTAT
       _____6E melon genomic DNA_____>

          -88         -78         -68         -58         -48         -38         -28         -18
          *           *           *           *           *           *           *           *
       AAATCTTAGA  AGCAACGTCT  TTACCGGAAT  CAACTCATTA  GGTATCCCAT  TTTCATCTAT  CAATTCACCC  TTGAAACTGC
       _____6E melon genomic DNA_____>


                         6E translational start site
                                  |
                              <6EMelNcoP
          -8          1 3        |
          *          * *         |
       TTTTCCCGGC  ACCGACT ATG GCC TC
       AAAAGGGCCG  aGGCTGg TAC CGG A
                        --NcoI--
       ____6E melon genomic DNA_____
```

box>

Fig. 6B

```
        -2442      -2432      -2422      -2412      -2402      -2392      -2382      -2372
          *          *          *          *          *          *          *          *
      AAGCTTGCAT GCCTGCAGGT CGACTCTAGA TCAATCAAAC ATTTATTTAA ATAGAACGTT TTAGTGGTTT TTGGATTTTA
      -Hind3
      _____pUC-19_____>
                                       _____2F melon genomic DNA_____>

        -2362      -2352      -2342      -2332      -2322      -2312      -2302      -2292
          *          *          *          *          *          *          *          *
      TTTATCTTTT TTATTATTTA CATTCAATTT AGATTTAACT CTTGCAGAAG ATGGAGGAAG AGAATTTTTA GAAATTGAAC
      _____2F melon genomic DNA_____>

        -2282      -2272      -2262      -2252      -2242      -2232      -2222      -2212
          *          *          *          *          *          *          *          *
      TGAAATAGAC TTAATTATTA AAAATCAAAA GAAAAATGGT GCCAACAAAG GTGACTAAGA GTGTAATGAA TTGGAATTAG
      _____2F melon genomic DNA_____>

        -2202      -2192      -2182      -2172      -2162      -2152      -2142      -2132
          *          *          *          *          *          *          *          *
      AACTTTCCTT CTGTATAGAT ATAATTGATG TTTTCCTTAA CTTTATTTTT ATGGTGGTTA TTTATTAATA ACTGAATTTT
      _____2F melon genomic DNA_____>

        -2122      -2112      -2102      -2092      -2082      -2072      -2062      -2052
          *          *          *          *          *          *          *          *
      TAAGAGTTCT TTTAATAACC AAATGTTATA GGATTCAATT GATTGTTTTA TGAGATTAGG CAAACACTTT ATATTGGAGA
      _____2F melon genomic DNA_____>

        -2042      -2032      -2022      -2012      -2002      -1992      -1982      -1972
          *          *          *          *          *          *          *          *
      AATAATTTAG TGTAGAAAGT AATTTTCATT TTGGATTGTT TAGATGAACA TCAAATCTTG CAACAACATT CAGTTAAGTA
      _____2F melon genomic DNA_____>

        -1962      -1952      -1942      -1932      -1922      -1912      -1902      -1892
          *          *          *          *          *          *          *          *
      TATATAAATA TATAGAGCCA CCAACCTCAA ATACAATATC TTCGGAAGCA AAATATTATA CATAATATGG AAAGAAGAGT
      _____2F melon genomic DNA_____>

        -1882      -1872      -1862      -1852      -1842      -1832      -1822      -1812
          *          *          *          *          *          *          *          *
      AGTACTGGTA CATGAATCTT ACGAAGAATT TAAGTATTAT TGGCTTTTCC AATGCAGAAG TCTCAACAAA TCACATTTTA
      _____2F melon genomic DNA_____>

        -1802      -1792      -1782      -1772      -1762      -1752      -1742      -1732
          *          *          *          *          *          *          *          *
      AAAACCGATT GAATAAACAT GCAAGTAAGA CTTTTGAAAA AACAAGCATT CAAACCTCAT ATCAATTATC TCTATATGCA
      _____2F melon genomic DNA_____>

        -1722      -1712      -1702      -1692      -1682      -1672      -1662      -1652
          *          *          *          *          *          *          *          *
      AAATGTTAGG TCAAATGAGT AATGAAATTA AGGACAAATC AACTAAAAAG AATCAATAAA GTGAATCGAA AAGAAACAAA
      _____2F melon genomic DNA_____>
```

Fig. 7A

```
        -1642       -1632       -1622       -1612       -1602       -1592       -1582       -1572
          *           *           *           *           *           *           *           *
      TATCAATCAA  ACCTAATGTA  TACGTGATTG  ATGATGCAGT  GTGTTTTGAG  ATATGGACAT  TTTGATAAAC  AACAAACCTC
      _____2F melon genomic DNA_____>


        -1562       -1552       -1542       -1532       -1522       -1512       -1502       -1492
          *           *           *           *           *           *           *           *
      CACTCCAATA  CGAGAAGAGA  GGCATTGAGT  GACAGATTAG  TGCCCTATTG  AAGAGGGTAA  GTCCAAAACA  AAACAAACAC
      _____2F melon genomic DNA_____>


        -1482       -1472       -1462       -1452       -1442       -1432       -1422       -1412
          *           *           *           *           *           *           *           *
      AAAACATGGT  GAAGAAATGT  TATGAATAAA  TGGCAGGGAA  AGACATGGTT  GTACATGTGG  TGTGAGTTTT  CTTCTTTCAA
      _____2F melon genomic DNA_____>


        -1402       -1392       -1382       -1372       -1362       -1352       -1342       -1332
          *           *           *           *           *           *           *           *
      ATCTGTGAAT  AAATTGGATT  ACGACCCAAC  AAGAGAAACA  CTGTTTGGAA  ACCATGACAG  GGCTACCCCA  TGGCGTGAAT
                                                                              —NcoI—
      _____2F melon genomic DNA_____>


        -1322       -1312       -1302       -1292       -1282       -1272       -1262       -1252
          *           *           *           *           *           *           *           *
      ATCAAGTATT  TAATTAATTA  AGCTCTCATC  CCCGCCATTC  GTTTTTTTAT  TCGATTCATA  TCTTATATTT  TATATACGAA
      _____2F melon genomic DNA_____>


        -1242       -1232       -1222       -1212       -1202       -1192       -1182       -1172
          *           *           *           *           *           *           *           *
      TAATTCTTGA  GTTTGATTTC  AATTTAGTTC  GTCAATAGTA  ATATTTTAAA  CTATGTTAAT  ATATAAAAAG  TAAATGCGAA
      _____2F melon genomic DNA_____>


        -1162       -1152       -1142       -1132       -1122       -1112       -1102       -1092
          *           *           *           *           *           *           *           *
      TGATTCTATT  AGTATTCACT  TTATATCACT  CCTTCTTAGA  GTAAAGTTTT  TAAAGTGGGA  AGGGAAATGG  AATACGACGT
      _____2F melon genomic DNA_____>


        -1082       -1072       -1062       -1052       -1042       -1032       -1022       -1012
          *           *           *           *           *           *           *           *
      GTGATTGGTA  GTTAAATTTC  CTTATCGACG  AGGTTACTGT  TTCCTTACTT  ATATATATGG  AGTCATCCTC  AATTTTTCAA
      _____2F melon genomic DNA_____>


        -1002        -992        -982        -972        -962        -952        -942        -932
          *           *           *           *           *           *           *           *
      CTCTCAACTT  CCAATTATAC  AAGCAAAACA  TTCAATACCA  TACATGCATC  TTTTTAGAAA  GAAAGAAGT  TCTCTCTTGG
      _____2F melon genomic DNA_____>


         -922        -912        -902        -892        -882        -872        -862        -852
          *           *           *           *           *           *           *           *
      ACTTTTTTTT  TCAATTCAAC  TATGCACCTT  TGTTATTTTA  GTTTTATAAT  TTTTGTTGTT  TCTTCCGTTT  AATCAAGTTG
      _____2F melon genomic DNA_____>
```

Fig. 7B

```
        -842        -832        -822        -812        -802        -792        -782        -772
         *           *           *           *           *           *           *           *
TTGTAATCAA CTTTATTGAT TCAAACACAT AGATATTTTG TTTAATAGTA TCAGTATATA ATAGGGTTAG AATAACCTTT
                            2F melon genomic DNA                                        >

        -762        -752        -742        -732        -722        -712        -702        -692
         *           *           *           *           *           *           *           *
CAAATATGTG TTTTTAAAAA ATCAAATCAC TTTAAAAATT AAAATATGTT TAATTAGTGT ATGTTTTTCT TTTTAAGTAT
                            2F melon genomic DNA                                        >

        -682        -672        -662        -652        -642        -632        -622        -612
         *           *           *           *           *           *           *           *
TAAACCACGA TAAAAAGTGC TTTAACACTT ATAAAAAATT AGATTAATTT AAAGGAAGTT GTCTGAACGG CAAAATTGAC
                            2F melon genomic DNA                                        >

        -602        -592        -582        -572        -562        -552        -542        -532
         *           *           *           *           *           *           *           *
AAAATATAAC AAAGTTTAAT GAACATTGTT CGAAATGTTT CGAAGAGGAA AGAAAACATT AAGTTTGAAA TATCTCGAGT
                            2F melon genomic DNA                                        >

        -522        -512        -502        -492        -482        -472        -462        -452
         *           *           *           *           *           *           *           *
TAAATACATA TCATCCCATA GTAATATATA ACAAAACAAA CTTAAATCTG AAAAAAAAAT TGATGTTAAT AAGAAAAAGA
                            2F melon genomic DNA                                        >

        -442        -432        -422        -412        -402        -392        -382        -372
         *           *           *           *           *           *           *           *
GATCAAACTC TTAATTTTTT AAAAAAATAA TGGTGAAAAA AACTGAAAAT TTTCCAATAT TGTTTAATTT CAAATTGATC
                            2F melon genomic DNA                                        >

        -362        -352        -342        -332        -322        -312        -302        -292
         *           *           *           *           *           *           *           *
CAAAAATTAA AGTTAAAAAA GCATTAAACA AAACAATTCA AAACCTAGCT ACTACACATT TACGAAAATA TATGATACAC
                            2F melon genomic DNA                                        >

        -282        -272        -262        -252        -242        -232        -222        -212
         *           *           *           *           *           *           *           *
AAAGGATTTT TGGGTGTAAA CATCTTTTTT ATTTTATATA CACCAAACTT CGTATATATT CACACATAAA GAAGGAAAAA
                            2F melon genomic DNA                                        >

        -202        -192        -182        -172        -162        -152        -142        -132
         *           *           *           *           *           *           *           *
GAATTAATGC AAGGGTGTGG CCAATTACGT ACCGTCGTCA TATCCTACTC ATCCGTTACG TTCTCAAATC TCTCTCTCTC
                            2F melon genomic DNA                                        >

        -122        -112        -102         -92         -82         -72         -62         -52
         *           *           *           *           *           *           *           *
CCTGCTCTCC TAATTATTTC TGCCAGCGAC CATATTTCAT TTTCAATTGT GTGTTTAAAA AGCCGAGAAT CGCAATCCTT
                            2F melon genomic DNA                                        >

                                                              Translational start site
        -42         -32         -22         -12          -2        |
         *           *           *           *           *        |
TTTCCTCCAC TCTTAATTCA TTTCCAATTC ACAAAAAT A G GATCCGCCAC CATGG
                                                  -BamHI-    -NcoI-
            2F melon genomic DNA                >
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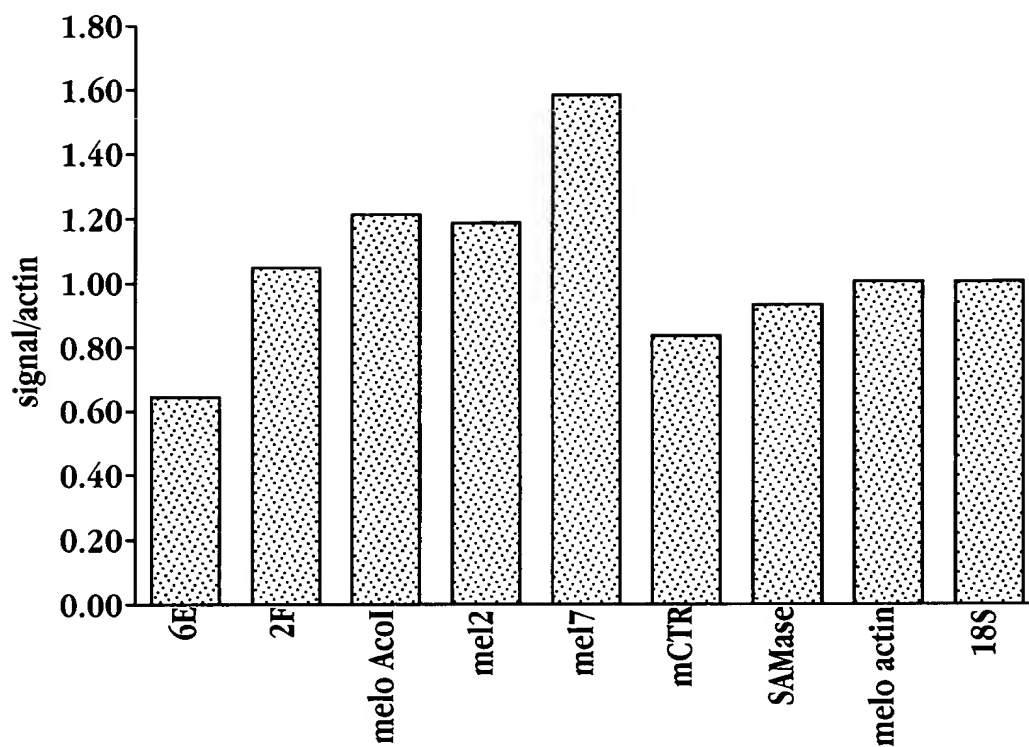
Fig. 7C

Fig. 8